

FILE 'MEDLINE, BIOSIS, EMBASE, SCISEARCH, CAPLUS, USPATFULL, PCTFULL'

ENTERED AT 15:13:18 ON 09 AUG 2006

L1 657493 S (INTERFERON OR IFN OR INF)  
L2 24717 S L1(S) (VARIANT OR MODIFI? OR SUBSTITUT?)  
L3 243 S L2(S) (HYDROPHOBIC OR (SOLVENT(W) EXPOSED))  
L4 239 DUP REM L3 (4 DUPLICATES REMOVED)  
L5 144 S L4 AND PY=<2003  
L6 131 S L1(S) F8  
L7 131 DUP REM L6 (0 DUPLICATES REMOVED)  
L8 83 S L7 AND PY=<2003  
L9 0 S AGUINALDO, ANNA/AU  
L10 0 S BEYNA, AMELIA/AU  
L11 0 S ANNA AGUINALDO/AU  
L12 7 S DESJARLAIS, JOHN/AU  
L13 84 S CHO, HO SUNG/AU  
L14 14 S MARSHALL, SHANNON/AU  
L15 22 S MUCHHAL, UMESH/AU  
L16 3 S VILLEGAS, MICHAEL/AU  
L17 15 S ZHUKOVSKY, EUGENE/AU  
L18 17 S (L13 OR L14 OR L15 OR L15 OR L16 OR L17) AND L2

## Refine Search

### Search Results -

Terms	Documents
(L6 or L7 or L8 or L9 or L10 or L11 or L13 or L14) and L2	19

Database:

US Pre-Grant Publication Full-Text Database  
 US Patents Full-Text Database  
 US OCR Full-Text Database  
 EPO Abstracts Database  
 JPO Abstracts Database  
 Derwent World Patents Index  
 IBM Technical Disclosure Bulletins

Search:

L15

Refine Search

Recall Text

Clear

Interrupt

### Search History

DATE: Wednesday, August 09, 2006   [Printable Copy](#)   [Create Case](#)

#### Set Name Query

side by side

#### Hit Count Set Name

result set

DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=OR

<u>L15</u>	(L6 or L7 or L8 or L9 or L10 or L11 or L13 or L14) and L2	19	<u>L15</u>
<u>L14</u>	"Zhukovsky, Eugene"[IN]	11	<u>L14</u>
<u>L13</u>	"Villegas, Michael"[IN]	4	<u>L13</u>
<u>L12</u>	"Aquino, Michael"[IN]	0	<u>L12</u>
<u>L11</u>	"Muchhal, Umesh"[IN]	16	<u>L11</u>
<u>L10</u>	"Marshall, Shannon"[IN]	24	<u>L10</u>
<u>L9</u>	"Desjarlais, John"[IN]	66	<u>L9</u>
<u>L8</u>	"Cho, Ho Sung"[IN]	15	<u>L8</u>
<u>L7</u>	"Beyna, Amelia"[IN]	4	<u>L7</u>
<u>L6</u>	"Aguinaldo, Anna"[IN]	6	<u>L6</u>
<u>L5</u>	L1 with F8	16	<u>L5</u>
<u>L4</u>	L2 same (hydrophobic or (solvent adj exposed))	52	<u>L4</u>
<u>L3</u>	L2 with (hydrophobic or (solvent adj exposed))	30	<u>L3</u>
<u>L2</u>	L1 with (variant or modifi\$7 or substitut\$4)	6559	<u>L2</u>

L1 (interferon or IFN or INF)

86531 L1

END OF SEARCH HISTORY

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:13:12 ; Search time 198 Seconds  
(without alignments)  
383.323 Million cell updates/sec

Title: US-10-676-705-15  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNIFYFINRLTGYLRLN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:22:12 ; Search time 51 Seconds  
(without alignments)  
284.904 Million cell updates/sec

Title: US-10-676-705-15  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:22:52 ; Search time 178 Seconds  
(without alignments)  
431.987 Million cell updates/sec

Title: US-10-676-705-15  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:23:52 ; Search time 29 Seconds  
(without alignments)  
327.467 Million cell updates/sec

Title: US-10-676-705-15  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNIFYFINRLTGYLRN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 204771 seqs, 57208143 residues

Total number of hits satisfying chosen parameters: 204771

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:17:07 ; Search time 39 Seconds  
(without alignments)  
409.538 Million cell updates/sec

Title: US-10-676-705-15  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.



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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:13:42 ; Search time 298 Seconds  
(without alignments)  
515.277 Million cell updates/sec

Title: US-10-676-705-15  
Perfect score: 874  
Sequence: 1 MSYNLLGFLQRSSNFQCQKL.....RVEILRNIFYFINRLTGYLRN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 11:59:17 ; Search time 195 Seconds  
(without alignments)  
389.220 Million cell updates/sec

Title: US-10-676-705-15-GLU8  
Perfect score: 873  
Sequence: 1 MSYNLLGELQRSSNFQCQKL.....RVEILRNFYFINRLTGYL RN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

OM protein - protein search, using sw model

Run on: July 15, 2006, 12:08:17 ; Search time 50 Seconds  
(without alignments)  
290.602 Million cell updates/sec

Title: US-10-676-705-15-GLU8  
Perfect score: 873  
Sequence: 1 MSYNLLGELQRSSNFQCQKL.....RVEILRNFYFINRLTGYL RN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

OM protein - protein search, using sw model

Run on: July 15, 2006, 12:08:57 ; Search time 186 Seconds  
(without alignments)  
413.407 Million cell updates/sec

Title: US-10-676-705-15-GLU8  
Perfect score: 873  
Sequence: 1 MSYNLLGELQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:09:57 ; Search time 27 Seconds  
(without alignments)  
351.724 Million cell updates/sec

Title: US-10-676-705-15-GLU8  
Perfect score: 873  
Sequence: 1 MSYNLLGELQRSSNFQCQKL.....RVEILRNIFYFINRLTGYLRN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 204771 seqs, 57208143 residues

Total number of hits satisfying chosen parameters: 204771

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

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OM protein - protein search, using sw model

Run on: July 15, 2006, 12:03:17 ; Search time 39 Seconds  
(without alignments)  
409.538 Million cell updates/sec

Title: US-10-676-705-15-GLU8  
Perfect score: 873  
Sequence: 1 MSYNLLGELQRSSNFQCQKL.....RVEILRNIFYFINRLTGYLRN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 15, 2006, 11:59:52 ; Search time 298 Seconds  
(without alignments)  
515.277 Million cell updates/sec

Title: US-10-676-705-15-GLU8  
Perfect score: 873  
Sequence: 1 MSYNLLGELQRSSNFQCQKL.....RVEILRNFYFINRLTGYLRLN 166

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.